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SEQUENCE LISTING

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NAKANISHI, HIROMI
OKI, HIROYUKI
YAMAGUCHI, HIROTAKA

<120> METHOD FOR TRANSFORMING PLANT, THE RESULTANT PLANT AND
GENE THEREOF

<130> 55022 (71526)

<140> 09/646,825

<141> 2000-09-22

<150> JP/10-96637

<151> 1998-03-24

<160> 38

<170> PatentIn Ver. 2.1

<210> 1

<211> 2092

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
saccharomyces cerevisiae

<220>

<221> CDS

<222> (20) .. (2077)

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1 5 10

atc tct ttc ttc gct aca gtc caa tcg agc gct aca ctc atc tcc act 100
Ile Ser Phe Phe Ala Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr
15 20 25

tca tgc att tct cag gct gca ctg tac cag ttc gga tgc tca agc aag 148
Ser Cys Ile Ser Gln Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys
30 35 40

tca aag tct tgc tac tgc aag aac atc aat tgg ctc gga agc gtc act 196
Ser Lys Ser Cys Tyr Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr
45 50 55

gca tgc gct tat gag aac tcc aaa tct aac aag act ctg gac tcc gct 244
Ala Cys Ala Tyr Glu Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala
60 65 70 75

ttg atg aaa ctt gcc agc caa tgc tca agt atc aag gtt tac aca ctg 292
 Leu Met Lys Leu Ala Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu
 80 85 90

gag gac atg aag aac atc tac ctt aat gca agt aac tac ctt cgc gct 340
 Glu Asp Met Lys Asn Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala
 95 100 105

cct gag aaa tcc gat aag aag aca gtt gtt tca caa ccg ttg atg gca 388
 Pro Glu Lys Ser Asp Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala
 110 115 120

aat gag acg gcc tat cac tac tac tat gag gaa aac tat ggg atc cac 436
 Asn Glu Thr Ala Tyr His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His
 125 130 135

ttg aat ttg atg cga tct caa tgg tgc gca tgg ggc ctc gtc ttc ttc 484
 Leu Asn Leu Met Arg Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe
 140 145 150 155

tgg gtc gca gtc ctt acc gcc gca act atc ttg aac att ctc aaa cgc 532
 Trp Val Ala Val Leu Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg
 160 165 170

gta ttc ggc aag aac att atg gca aat tct gtt aag aag tct ctt atc 580
 Val Phe Gly Lys Asn Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile
 175 180 185

tac cca agc gtt tac aaa gac tac aac gag aga act ttc tat ctt tgg 628
 Tyr Pro Ser Val Tyr Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp
 190 195 200

aaa cgt ttg cca ttc aac ttt aca act cga ggc aaa gga ctc gta gtt 676
 Lys Arg Leu Pro Phe Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val
 205 210 215

ctt atc ttt gtc att ctg act att ctc tca ctc tct ttc gga cat aac 724
 Leu Ile Phe Val Ile Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn
 220 225 230 235

atc aag ttg cca cat cct tac gat aga cct aga tgg aga aga tca atg 772
 Ile Lys Leu Pro His Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met
 240 245 250

gca ttc gtc tca cgc cgt gct gac ttg atg gca atc gct ctt ttc ccc 820
 Ala Phe Val Ser Arg Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro
 255 260 265

gtg gtg tac ctt ttc ggt atc cgg aac aac ccc ttc atc cca atc acc 868
 Val Val Tyr Leu Phe Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr
 270 275 280

gga ttg agc ttt agt act ttc aac ttt tac cac aaa tgg tca gca tac 916
 Gly Leu Ser Phe Ser Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr
 285 290 295

A¹

gtc tgc ttc atg tta gcc gtc gtc cat tca atc gtt atg acc gct tca	964
Val Cys Phe Met Leu Ala Val Val His Ser Ile Val Met Thr Ala Ser	
300 305 310 315	
gga gtt aaa cga gga gta ttc cag tct ctt gta agg aaa ttc tac ttc	1012
Gly Val Lys Arg Gly Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe	
320 325 330	
aga tgg gga ata gta gcc aca att ctt atg tcc atc atc att ttc cag	1060
Arg Trp Gly Ile Val Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln	
335 340 345	
tcc gag aag gtc ttc agg aac cga ggt tat gaa atc ttc tta ctt att	1108
Ser Glu Lys Val Phe Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile	
350 355 360	
cac aaa gcc atg aac atc atg ttt atc ata gct atg tat tac cat tgc	1156
His Lys Ala Met Asn Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys	
365 370 375	
cac aca cta gga tgg atg ggc tgg atc tgg tcc atg gct ggc atc ctc	1204
His Thr Leu Gly Trp Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu	
380 385 390 395	
tgc ttc gac agg ttc tgc cga att gta cgt atc atc atg aac gga ggt	1252
Cys Phe Asp Arg Phe Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly	
400 405 410	
ctt aag acc gcc act ttg tgc acc aca gat gat tct aac gtt atc aag	1300
Leu Lys Thr Ala Thr Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys	
415 420 425	
atc tct gtc aag aag cct aag ttc ttc aag tat caa gtg gga gca ttt	1348
Ile Ser Val Lys Lys Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe	
430 435 440	
gcc tat atg tac ttt ctt tca cca aaa tca gcc tgg ttc tac agt ttt	1396
Ala Tyr Met Tyr Phe Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe	
445 450 455	
caa tct cat ccc ttc aca gtc cta tca gaa agg cac aga gat cct aac	1444
Gln Ser His Pro Phe Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn	
460 465 470 475	
aac cca gat caa cta act atg tac gtc aaa gct aac aag ggc att acg	1492
Asn Pro Asp Gln Leu Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr	
480 485 490	
aga gta ctt ctt agc aaa gtt cta agc gct cca aac cat acc gtt gat	1540
Arg Val Leu Leu Ser Lys Val Leu Ser Ala Pro Asn His Thr Val Asp	
495 500 505	
tgc aag att ttc tta gag gga cca tat ggc gta act gtc cct cac att	1588
Cys Lys Ile Phe Leu Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile	
510 515 520	

gcc aaa ctt aag aga aat cta gta gga gta gct gcg ggc ctc ggc gtg 1636
 Ala Lys Leu Lys Arg Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val
 525 530 535

gca gcc atc tac ccc cat ttc gta gaa tgc ctt aga ttg cct agc act 1684
 Ala Ala Ile Tyr Pro His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr
 540 545 550 555

gat caa ctg cag cac aag ttc tac tgg atc gtc aac gac ctt agt cac 1732
 Asp Gln Leu Gln His Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His
 560 565 570

ctt aag tgg ttc gaa aac gag cta caa tgg ctt aag gag aaa tct tgt 1780
 Leu Lys Trp Phe Glu Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys
 575 580 585

gaa gtc tct gtc atc tac act ggg tca tca gtg gag gat aca aac tca 1828
 Glu Val Ser Val Ile Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser
 590 595 600

gat gag tcc act aag ggt ttc gat gac aag gaa gaa tct gaa atc acc 1876
 Asp Glu Ser Thr Lys Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr
 605 610 615

gta gaa tgc ctt aac aag agg cca gac ctc aaa gag cta gtg aga tca 1924
 Val Glu Cys Leu Asn Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser
 620 625 630 635

gag atc aaa ttg tca gaa ctc gag aac aac aac atc act ttc tac tca 1972
 Glu Ile Lys Leu Ser Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser
 640 645 650

tgc gga cca gcg act ttc aat gac gac ttt agg aat gca gtt gta caa 2020
 Cys Gly Pro Ala Thr Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln
 655 660 665

ggt atc gat tct agt ctg aag ata gat gtc gaa cta gag gag gag agt 2068
 Gly Ile Asp Ser Ser Leu Lys Ile Asp Val Glu Leu Glu Glu Glu Ser
 670 675 680

ttt act tgg taagagctca agctt 2092
 Phe Thr Trp
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<210> 2

<211> 686

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 saccharomyces cerevisiae

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Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr Ser Cys Ile Ser Gln
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 Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys Ser Lys Ser Cys Tyr
 35 40 45
 Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr Ala Cys Ala Tyr Glu
 50 55 60
 Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala Leu Met Lys Leu Ala
 65 70 75 80
 Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu Glu Asp Met Lys Asn
 85 90 95
 Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala Pro Glu Lys Ser Asp
 100 105 110
 Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala Asn Glu Thr Ala Tyr
 115 120 125
 His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His Leu Asn Leu Met Arg
 130 135 140
 Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe Trp Val Ala Val Leu
 145 150 155 160
 Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg Val Phe Gly Lys Asn
 165 170 175
 Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr
 180 185 190
 Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe
 195 200 205
 Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile
 210 215 220
 Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
 225 230 235 240
 Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met Ala Phe Val Ser Arg
 245 250 255
 Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro Val Val Tyr Leu Phe
 260 265 270
 Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr Gly Leu Ser Phe Ser
 275 280 285
 Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr Val Cys Phe Met Leu
 290 295 300
 Ala Val Val His Ser Ile Val Met Thr Ala Ser Gly Val Lys Arg Gly
 305 310 315 320

Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe Arg Trp Gly Ile Val
 325 330 335
 Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln Ser Glu Lys Val Phe
 340 345 350
 Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile His Lys Ala Met Asn
 355 360 365
 Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys His Thr Leu Gly Trp
 370 375 380
 Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu Cys Phe Asp Arg Phe
 385 390 395 400
 Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly Leu Lys Thr Ala Thr
 405 410 415
 Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys Ile Ser Val Lys Lys
 420 425 430
 Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe Ala Tyr Met Tyr Phe
 435 440 445
 Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe Gln Ser His Pro Phe
 450 455 460
 Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn Asn Pro Asp Gln Leu
 465 470 475 480
 Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr Arg Val Leu Leu Ser
 485 490 495
 Lys Val Leu Ser Ala Pro Asn His Thr Val Asp Cys Lys Ile Phe Leu
 500 505 510
 Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile Ala Lys Leu Lys Arg
 515 520 525
 Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val Ala Ala Ile Tyr Pro
 530 535 540
 His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr Asp Gln Leu Gln His
 545 550 555 560
 Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His Leu Lys Trp Phe Glu
 565 570 575
 Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys Glu Val Ser Val Ile
 580 585 590
 Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser Asp Glu Ser Thr Lys
 595 600 605
 Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr Val Glu Cys Leu Asn
 610 615 620

Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser Glu Ile Lys Leu Ser
 625 630 635 640

Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser Cys Gly Pro Ala Thr
 645 650 655

Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln Gly Ile Asp Ser Ser
 660 665 670

Leu Lys Ile Asp Val Glu Leu Glu Glu Ser Phe Thr Trp
 675 680 685

<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 3
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17

<210> 4
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 4
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24

<210> 5
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 cttcgctaca gtccaatcga gcg 83

<210> 6
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
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 ttcggatgct caagcaagtc aaa 83

<210> 7
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
 caagcaagtc aaagtcttgc tactgcaaga acatcaattg gtcggaagc gtcactgcat 60
 gcgcttatga gaactccaaa tct 83

<210> 8
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 8
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 agagtcttgt tagatttgga gtt 83

<210> 9
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 9
 tgtcttctta tcggatttct caggagcgcg aaggtagtta cttgcattaa ggtagatggt 60
 cttcatgtcc tccagtgtgt aaa 83

<210> 10
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 10
 ggatcccata gttttcctca tagtagtagt gataggccgt ctcatttgcc atcaacgggtt 60
 gtgaaacaac tgtcttctta tcg 83

<210> 11

<211> 80
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11
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 tcgcagtctt taccgccgca 80

<210> 12
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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 aaattctgtt aagaagtctc 80

<210> 13
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13
 gttaagaagt ctcttatcta cccaagcgtt tacaagact acaacgagag aactttctat 60
 ctttggaac gtttgccatt 80

<210> 14
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14
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 taaagttgaa tggcaaactg 80

<210> 15
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15
aatgccattg atctttctcca tctaggtcta tcgtaaggat gtggcaactt gatggttatgt 60
ccgaaagaga gtgagagaat 80

<210> 16
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
tccggatacc gaaaaggtac accacgggga aaagagcgat tgccatcaag tcagcacggc 60
gtgagacgaa tgccattgat 80

<210> 17
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
tccggaacaa ccccttcac ccaatcacgc gattgagctt tagtactttc aactttttacc 60
acaaatggtc agcatagtc tgc 83

<210> 18
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
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aaacgaggag tattccagtc tct 83

<210> 19
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
tattccagtc tcttgtaagg aaattctact tcagatgggg aatagtagcc acaattctta 60
tgtccatcat cattttccag tcc 83

<210> 20
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
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 aagaccttct cggactggaa aat 83

<210> 21
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
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<210> 22
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 gtcgacaaag tggcgggtctt aagacctccg ttcattgatga tacgtacaat tcggcagaac 60
 ctgtcgaagc agaggatgcc agc 83

<210> 23
 <211> 82
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
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 gtatcaagtg ggagcatttg cc 82

<210> 24
 <211> 82
 <212> DNA
 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 24

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tctcatcct tcacagtcct at 82

<210> 25

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25

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gtcaaagcta acaagggcat ta 82

<210> 26

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 26

cctctaagaa aatcttgcaa tcaacggat ggtttggagc gcttagaact ttgctaagaa 60
gtactctcgt aatgcccttg tt 82

<210> 27

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 27

ggccccgcagc tactcctact agatttctct taagtttggc aatgtgaggg acagttacgc 60
catatggtcc ctctaagaaa at 82

<210> 28

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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cacgccgagg cccgcagcta ct 82

<210> 29
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 29
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 gagctacaat ggcttaa 77

<210> 30
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 30
 acaatggctt aaggagaaat cttgtgaagt ctctgtcatc tacactgggt catcagtgga 60
 ggatacaaac tcagatg 77

<210> 31
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 31
 caaactcaga tgagtccact aagggtttcg atgacaagga agaattctgaa atcaccgtag 60
 aatgccttaa caagagg 77

<210> 32
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 32
 gtgatgttgt tggtctcgag ttctgacaat ttgatctctg atctcactag ctctttgagg 60
 tctggcctct tgtaag 77

<210> 33
 <211> 77
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

cgataccttg tacaactgca ttcctaaagt cgtcattgaa agtcgctggt ccgcatgagt 60
 agaaagtgat gttgttg 77

<210> 34

<211> 77

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 34

aagcttgagc tcttaccaag taaaactctc ctctcttagt tcgacatcta tcttcagact 60
 agaatcgata ccttgta 77

<210> 35

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 35

gactcgagtc gacatcgatt tttttttttt ttttt 35

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<211> 2059

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 36

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 tctagtaaat ctaaaagttg ctactgtaaa aacatcaatt ggctgggttc agtgacagca 180
 tgtgcctatg agaattccaa atctaacaaa acactagaca gcgccttaat gaagtttagca 240
 tcccaatggt caagcatcaa agtttatact ttagaggaca tgaagaatat ttattttaat 300
 gcgtcaaatt atttgagagc acctgagaaa agtgataaaa aaaccgtggt tagtcaaccg 360
 ctcatggcga acgagacagc gtatcattat tattatgagg aaaattatgg tatccatctt 420
 aacctaatgc gctctcaatg gtgcgcttggt ggtctcgtct tcttctgggt ggggtgtgctt 480
 actgcagcca ctatcttgaa cattctgaaa aggggtgtttg gtaagaacat catggcaaac 540
 tccgtcaaaa aatcacttat ttatccttct gtttacaag attataatga acgaactttt 600
 tatttatgga agcgtctacc atttaatttt acaactcgag gcaagggtct cgtcgtatta 660
 atttttgtta ttttgactat attatctctc agttttggtc ataataatta acttccacac 720
 ccatatgata ggcccagatg gagaagaagt atggcctttg tgagtcgtag agcagacttg 780
 atggccattg cacttttccc agtagtctat ctattcggaa taagaaataa tcccttcac 840
 cctataacag ggctttcctt ttctacattt aatttctatc ataaatggtc tgcctacgtt 900
 tgtttcatgt tgccggttggt acactcaatt gtcattgacc cctcgggagt gaaaagaggt 960
 gtgtttcaaa gtctgggttag gaaattttac tttagggtgg gtatagtggc aacgatatta 1020
 atgtctatta ttattttcca aagtgaacaaa gtatttagaa atagagggtg tgagatatct 1080
 cttcttattc ataaagcgat gaatattatg ttcattattg ccatgtacta ccattgtcac 1140

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Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe Asn Phe Thr Thr
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Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile Leu Thr Ile Leu
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50 55 60

A²